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O | O IntelliGenetics  
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GENALIGN - Multiple Sequence Alignment Program  
Release 5.4

Wed 12 Jan 105 12:57:02 -PST

Solution Parameters:

Amino Alphabet = Identity  
Output line length = 80  
Compress = Off  
Histogram = Off  
Randomization = Off  
AMINO-Res-length = 5.00  
DEletion-weight = 5.00  
Length-factor = 0  
Matching-weight = 1.00  
NUCelic-Res-length = 4  
Spread-factor = 50

Amino Acids 1 - 1531 (HDR)  
= SEQ ID NO: 1 or 5,760,880  
(for example)  
or A Aw S74 860  
1532 - 1537 = 6 glycine spacer

Clustered order of selected sequences:

8. US-10-665-283-8 (1-1947)  
1. US-10-665-283-1 (1-1927)  
6. US-10-665-283-6 (1-1891)  
4. US-10-665-283-4 (1-1891)

Region Alignment: (listed in clustered order)

US-10-665- 1 MALRGFCSDGSQDPIWDNYTNTNSNPDTIKCFONTVLWVPCPFYLWACFPFFFLYLSRHD  
1 MALRGFCSDGSQDPIWDNYTNTNSNPDTIKCFONTVLWVPCPFYLWACFPFFFLYLSRHD  
1 MALRGFCSDGSQDPIWDNYTNTNSNPDTIKCFONTVLWVPCPFYLWACFPFFFLYLSRHD  
1 MALRGFCSDGSQDPIWDNYTNTNSNPDTIKCFONTVLWVPCPFYLWACFPFFFLYLSRHD  
consensus MALRGFCSDGSQDPIWDNYTNTNSNPDTIKCFONTVLWVPCPFYLWACFPFFFLYLSRHD  
US-10-665- 62 RGYIQTPLAKTKTAFLGFLIWTCAFLDFYSFWEBSRGIFLAPVFLVSPTLGTTLATF  
62 RGYIQTPLAKTKTAFLGFLIWTCAFLDFYSFWEBSRGIFLAPVFLVSPTLGTTLATF  
US-10-665- 62 RGYIQTPLAKTKTAFLGFLIWTCAFLDFYSFWEBSRGIFLAPVFLVSPTLGTTLATF  
US-10-665- 62 RGYIQTPLAKTKTAFLGFLIWTCAFLDFYSFWEBSRGIFLAPVFLVSPTLGTTLATF  
consensus RGYIQTPLAKTKTAFLGFLIWTCAFLDFYSFWEBSRGIFLAPVFLVSPTLGTTLATF  
US-10-665- 123 LIQLERKGVOSSGIMLTFLWVALCALA1RSKIMTALKEDAQVLDLFRDITFYFSLL  
US-10-665- 123 LIQLERKGVOSSGIMLTFLWVALCALA1RSKIMTALKEDAQVLDLFRDITFYFSLL  
US-10-665- 123 LIQLERKGVOSSGIMLTFLWVALCALA1RSKIMTALKEDAQVLDLFRDITFYFSLL  
US-10-665- 123 LIQLERKGVOSSGIMLTFLWVALCALA1RSKIMTALKEDAQVLDLFRDITFYFSLL  
consensus LIQLERKGVOSSGIMLTFLWVALCALA1RSKIMTALKEDAQVLDLFRDITFYFSLL  
US-10-665- 184 IQLVLSCFSDRSPFLSETIDHDPNPCESSASFSLRITEFWNTGLIVGRQPLEGDSLNL  
US-10-665- 184 IQLVLSCFSDRSPFLSETIDHDPNPCESSASFSLRITEFWNTGLIVGRQPLEGDSLNL  
US-10-665- 184 IQLVLSCFSDRSPFLSETIDHDPNPCESSASFSLRITEFWNTGLIVGRQPLEGDSLNL

Search Notes

US-10-665- consensus	184 IQLVLSCFSDRSPFLSETIDHDPNPCESSASFSLRITEFWNTGLIVGRQPLEGDSLNL
US-10-665- consensus	245 NKEDTSEQVQVPUVQKWKKECACTRKOPKVYSSKDPQPKESSKVDANEVEALIVKSP
US-10-665- consensus	NKEDTSEQVQVPUVQKWKKECACTRKOPKVYSSKDPQPKESSKVDANEVEALIVKSP
US-10-665- consensus	306 QKEWNPSPLFKVLYKTFGPYPLMSFFPKA1HDLMMFSGPQ1KL1LKFKVNDTKAPDWQGYF
US-10-665- consensus	367 TVLLFTTACIQLTVLHQYFHICFVSGMIRKTTAVIGAVYRKA1VITNSARKSSTVGEIVNL
US-10-665- consensus	428 SYDAQRPMFLATYINNIWSPAPQVIALYLWLN1LGPSPVLAGVAVNLMYFVNAYMAMKTK
US-10-665- consensus	489 TYQVAMHKSKDRIKLMNEILNGIKVLYAWBLAFDKVLA1ROBELLKVKKSAYLSAVG
US-10-665- consensus	550 TFTWVCTPFLVALCTFAYVVTIDENNI1LRFPLN1LPVVISSIVQAS
US-10-665- consensus	TFTWVCTPFLVALCTFAYVVTIDENNI1LRFPLN1LPVVISSIVQAS
US-10-665- consensus	611 VSLKRLRFLSHEELEPDSTERPVKDGGTNS1TVRNATFWA5DPTLNGITS1PEG

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US-10-665-	611	VSLKRRIPLSHEELPDTSIERRPVKDGCGTNSITVRNATFTWARSDDPPTLNGITFISPEG	US-10-665-	1038	SIGGILASRCLHYDLHSLRSPSKEDDTDSMIEVYIKMFENGSL
US-10-665-	611	VSLKRRIPLSHEELPDTSIERRPVKDGCGTNSITVRNATFTWARSDDPPTLNGITFISPEG	US-10-665-	1038	SIGGILASRCLHYDLHSLRSPSKEDDTDSMIEVYIKMFENGSL
US-10-665-	611	VSLKRRIPLSHEELPDTSIERRPVKDGCGTNSITVRNATFTWARSDDPPTLNGITFISPEG	US-10-665-	1038	SIGGILASRCLHYDLHSLRSPSKEDDTDSMIEVYIKMFENGSL
consensus		VSLKRRIPLSHEELPDTSIERRPVKDGCGTNSITVRNATFTWARSDDPPTLNGITFISPEG	US-10-665-	1038	SIGGILASRCLHYDLHSLRSPSKEDDTDSMIEVYIKMFENGSL
US-10-665-	672	ALVAVVQVGCKSSLLSALLAEMDVKVEGHIAKGSAVYQQAWQNDSLIRENTLFGCQL	US-10-665-	1099	FNVIGACTVILLATPIAAIIIPPIGLIYFFVQRFYVASSRQLRKLESVRSRSPYSSHNETL
US-10-665-	672	ALVAVVQVGCKSSLLSALLAEMDVKVEGHIAKGSAVYQQAWQNDSLIRENTLFGCQL	US-10-665-	1099	FNVIGACTVILLATPIAAIIIPPIGLIYFFVQRFYVASSRQLRKLESVRSRSPYSSHNETL
US-10-665-	672	ALVAVVQVGCKSSLLSALLAEMDVKVEGHIAKGSAVYQQAWQNDSLIRENTLFGCQL	US-10-665-	1099	FNVIGACTVILLATPIAAIIIPPIGLIYFFVQRFYVASSRQLRKLESVRSRSPYSSHNETL
consensus		ALVAVVQVGCKSSLLSALLAEMDVKVEGHIAKGSAVYQQAWQNDSLIRENTLFGCQL	US-10-665-	1099	FNVIGACTVILLATPIAAIIIPPIGLIYFFVQRFYVASSRQLRKLESVRSRSPYSSHNETL
US-10-665-	733	EPPYYRSVIQACALLPDLIELPSGDTBEIGEKVNLSGGOKQRVSALARAYSNADYLFLDD	consensus		FNVIGACTVILLATPIAAIIIPPIGLIYFFVQRFYVASSRQLRKLESVRSRSPYSSHNETL
US-10-665-	733	EPPYYRSVIQACALLPDLIELPSGDTBEIGEKVNLSGGOKQRVSALARAYSNADYLFLDD	US-10-665-	1160	LGVSYTRAFEEQERFIHQSDLKYDENOKAYPSIVANRWLAVRLECVGNCIVLFAALFAVI
US-10-665-	733	EPPYYRSVIQACALLPDLIELPSGDTBEIGEKVNLSGGOKQRVSALARAYSNADYLFLDD	US-10-665-	1160	LGVSYTRAFEEQERFIHQSDLKYDENOKAYPSIVANRWLAVRLECVGNCIVLFAALFAVI
US-10-665-	733	EPPYYRSVIQACALLPDLIELPSGDTBEIGEKVNLSGGOKQRVSALARAYSNADYLFLDD	US-10-665-	1160	LGVSYTRAFEEQERFIHQSDLKYDENOKAYPSIVANRWLAVRLECVGNCIVLFAALFAVI
consensus		EPPYYRSVIQACALLPDLIELPSGDTBEIGEKVNLSGGOKQRVSALARAYSNADYLFLDD	US-10-665-	1160	LGVSYTRAFEEQERFIHQSDLKYDENOKAYPSIVANRWLAVRLECVGNCIVLFAALFAVI
US-10-665-	794	PLSAVDAHVGKHI FENVIGPKMLKNTRILVTHSMSYLPQVDVTIVMSGKKISEMGSYQE	consensus		LGVSYTRAFEEQERFIHQSDLKYDENOKAYPSIVANRWLAVRLECVGNCIVLFAALFAVI
US-10-665-	794	PLSAVDAHVGKHI FENVIGPKMLKNTRILVTHSMSYLPQVDVTIVMSGKKISEMGSYQE	US-10-665-	1221	SRHSLSAGLVGLSVSLSQVTTINWLVRMSSMETNIVAVERLKEYSETEKEAPWQIQT
US-10-665-	794	PLSAVDAHVGKHI FENVIGPKMLKNTRILVTHSMSYLPQVDVTIVMSGKKISEMGSYQE	US-10-665-	1221	SRHSLSAGLVGLSVSLSQVTTINWLVRMSSMETNIVAVERLKEYSETEKEAPWQIQT
US-10-665-	794	PLSAVDAHVGKHI FENVIGPKMLKNTRILVTHSMSYLPQVDVTIVMSGKKISEMGSYQE	US-10-665-	1221	SRHSLSAGLVGLSVSLSQVTTINWLVRMSSMETNIVAVERLKEYSETEKEAPWQIQT
consensus		PLSAVDAHVGKHI FENVIGPKMLKNTRILVTHSMSYLPQVDVTIVMSGKKISEMGSYQE	US-10-665-	1221	SRHSLSAGLVGLSVSLSQVTTINWLVRMSSMETNIVAVERLKEYSETEKEAPWQIQT
US-10-665-	855	Llardgafaaeflirtyasteqodaaengvtgvsgpkreakomengmlvtdsagkkqlqrqsl	consensus		SRHSLSAGLVGLSVSLSQVTTINWLVRMSSMETNIVAVERLKEYSETEKEAPWQIQT
US-10-665-	855	Llardgafaaeflirtyasteqodaaengvtgvsgpkreakomengmlvtdsagkkqlqrqsl	US-10-665-	1282	APSSWPQGVREFRNYCLRYREDLDFVLRHINTVTINGGEKVIVGRTGAKSSLTGLFR
US-10-665-	855	Llardgafaaeflirtyasteqodaaengvtgvsgpkreakomengmlvtdsagkkqlqrqsl	US-10-665-	1282	APSSWPQGVREFRNYCLRYREDLDFVLRHINTVTINGGEKVIVGRTGAKSSLTGLFR
US-10-665-	855	Llardgafaaeflirtyasteqodaaengvtgvsgpkreakomengmlvtdsagkkqlqrqsl	US-10-665-	1282	APSSWPQGVREFRNYCLRYREDLDFVLRHINTVTINGGEKVIVGRTGAKSSLTGLFR
consensus		Llardgafaaeflirtyasteqodaaengvtgvsgpkreakomengmlvtdsagkkqlqrqsl	US-10-665-	1282	APSSWPQGVREFRNYCLRYREDLDFVLRHINTVTINGGEKVIVGRTGAKSSLTGLFR
US-10-665-	916	SSSSYSGDISRHINSTAELOKAEEAKBETWKMEADKAQTGQVKSIVYDYMKAICLFISF	consensus		APSSWPQGVREFRNYCLRYREDLDFVLRHINTVTINGGEKVIVGRTGAKSSLTGLFR
US-10-665-	916	SSSSYSGDISRHINSTAELOKAEEAKBETWKMEADKAQTGQVKSIVYDYMKAICLFISF	US-10-665-	1343	INESAGEIIIDGINIAKIGLHDLRFKITTIPQDPVLFGCSLRLNLDPFSQYSDEBVWTSL
US-10-665-	916	SSSSYSGDISRHINSTAELOKAEEAKBETWKMEADKAQTGQVKSIVYDYMKAICLFISF	US-10-665-	1343	INESAGEIIIDGINIAKIGLHDLRFKITTIPQDPVLFGCSLRLNLDPFSQYSDEBVWTSL
US-10-665-	916	SSSSYSGDISRHINSTAELOKAEEAKBETWKMEADKAQTGQVKSIVYDYMKAICLFISF	US-10-665-	1343	INESAGEIIIDGINIAKIGLHDLRFKITTIPQDPVLFGCSLRLNLDPFSQYSDEBVWTSL
consensus		SSSSYSGDISRHINSTAELOKAEEAKBETWKMEADKAQTGQVKSIVYDYMKAICLFISF	US-10-665-	1343	INESAGEIIIDGINIAKIGLHDLRFKITTIPQDPVLFGCSLRLNLDPFSQYSDEBVWTSL
US-10-665-	977	LSIFLFMCHNVSALASNWTSLMTDPVNGTOEHTKVLSTYGAAGISQGIAVFGYSMAV	consensus		INESAGEIIIDGINIAKIGLHDLRFKITTIPQDPVLFGCSLRLNLDPFSQYSDEBVWTSL
US-10-665-	977	LSIFLFMCHNVSALASNWTSLMTDPVNGTOEHTKVLSTYGAAGISQGIAVFGYSMAV	US-10-665-	1404	ELAHLKDFVSAIPDKLHDHEAGGENLSVGQRQLVCLARLRTKILVDEATAVDELT
US-10-665-	977	LSIFLFMCHNVSALASNWTSLMTDPVNGTOEHTKVLSTYGAAGISQGIAVFGYSMAV	US-10-665-	1404	ELAHLKDFVSAIPDKLHDHEAGGENLSVGQRQLVCLARLRTKILVDEATAVDELT
US-10-665-	977	LSIFLFMCHNVSALASNWTSLMTDPVNGTOEHTKVLSTYGAAGISQGIAVFGYSMAV	US-10-665-	1404	ELAHLKDFVSAIPDKLHDHEAGGENLSVGQRQLVCLARLRTKILVDEATAVDELT

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US-10-665- 1404	ELAHLKDFVSAALPDKLDHECLEGGENLSVGQOLYCLARALLRKTKILVDEATAVDLET	
consensus	DLIQCOSTIRTQFEDCTVLTAHRLNTIMDYTRVTLDKGBIQEYGAPS DLLQQRGLFYSMA	
US-10-665- 1465	DLIQCOSTIRTQFEDCTVLTAHRLNTIMDYTRVTLDKGBIQEYGAPS DLLQQRGLFYSMA	
consensus	DLIQCOSTIRTQFEDCTVLTAHRLNTIMDYTRVTLDKGBIQEYGAPS DLLQQRGLFYSMA	
US-10-665- 1526	KDAGLUVGGGGGMUSRKG1PEEYVLU TRIAEDPAEPYRTRERRARFYSKKGNCNVAKHN1	
consensus	KDAGLUVGGGGGMUSRKG1PEEYVLU TRIAEDPAEPYRTRERRARFYSKKGNCNVAKHN1	
US-10-665- 1587	REQGRFLQDVFTLVDLKMPHTLLIIFTMSFLCSWLLFAMVWNLIAFAHGDLYaymekgktd	
consensus	REQGRFLQDVFTLVDLKMPHTLLIIFTMSFLCSWLLFAMVWNLIAFAHGDLYaymekgktd	
US-10-665- 1648	1APrypydypdyageGTNVPCTSIHSFSSAFLFSIEVQVTIGFGGRMVTECPLAIIILIV	
US-10-665- 1638	Ap	
consensus	1APrypydypdyageGTNVPCTSIHSFSSAFLFSIEVQVTIGFGGRMVTECPLAIIILIV	
US-10-665- 1709	QNIVGLMINAINMGC1FMKTAQHRAETLIFSKHAYTILRGRLCFMLRYGDLRKSMSIIS	
US-10-665- 1689	QNIVGLMINAINMGC1FMKTAQHRAETLIFSKHAYTILRGRLCFMLRYGDLRKSMSIIS	
consensus	QNIVGLMINAINMGC1FMKTAQHRAETLIFSKHAYTILRGRLCFMLRYGDLRKSMSIIS	
US-10-665- 1770	ATIHMQVVRKTTSPEGEVVPLHQVD1PMENGCGNG1FLVAPLITYHVIDNSPLYDLAPS	
US-10-665- 1750	ATIHMQVVRKTTSPEGEVVPLHQVD1PMENGCGNG1FLVAPLITYHVIDNSPLYDLAPS	
consensus	ATIHMQVVRKTTSPEGEVVPLHQVD1PMENGCGNG1FLVAPLITYHVIDNSPLYDLAPS	
US-10-665- 1831	DHHHQDLEIIVILEGVETTGITOARTSYLADEILWGORPVPIVAEDGRSVSDYSGKFG	

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